## SEQUENCE LISTING

<110> University of Florida Research Foundation, Inc. Hannah, L. Curtis Lyerly Linebarger, Carla R.

- <120> Heat Stable Variants of Adenosine Diphosphate Glucose Pyrophosphorylase
- <130> UF-371XC1 PCT
- <150> US 60/496,188
- <151> 2003-08-18
- <160> 42
- <170> PatentIn version 3.2
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Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys 50 60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile 65 70 75 80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr 85 90 95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg 100 105 110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu 115 120 125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
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Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr 180 185 190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu 195 200 205

Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro 210 215 220

Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly 225 230 235 240

Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly

245 250 255

Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln 260 265 270

Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr 275 280 285

Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu 290 295 300

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<223> Shrunken-2 gene revertant form

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ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct
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Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat
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Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
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Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
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Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
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	act ctt cat Thr Leu His		_				243
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Ala Asp Ala 80	Asn Arg Val	Ser Ala 85	Ile Ile	Leu Gly 90	Gly Gly	Thr Gly	
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<222> (1578)
<223> k = g or t.
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cag ata aga tot tgt gag ggt gat ggg att gac agg ttg gaa aaa tta
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15
                      20
                                           25
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                  35
ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct
                                                                     195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
                                  55
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat
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Cys	Pro	Glu 65	Thr	Leu	His	Ser	Gln 70	Thr	Gln	Ser	Ser	Arg 75	Lys	Asn	Tyr	
gct	gat	gca	aac	cgt	gta	tct	gck	atc	att	ttg	ggc	gga	ggc	act	gga	291
Ala	Asp 80	Ala	Asn	Arg	Val	Ser 85	Ala	Ile	Ile	Leu	Gly 90	Gly	Gly	Thr	Gly	
	_				_		_		aga Arg		_		-			339
									atc Ile 120							387
	-				_				atg Met							435
									tac Tyr							483
	-	-							gcg Ala							531
						_			gca Ala							579
					_			-	cac His 200				_			627
_		_	_		_	_			cgg Arg	_			_	_		675
									gat Asp							723
	_	_		_	-				aat Asn				_			771
			_	-					gaa Glu							819
									ttc Phe 280							867

	gca Ala									915
	aaa Lys									963
	gac Asp 320			_						1011
	cag Gln									1059
	tca Ser		-							1107
	gat Asp									1155
_	cct Pro									1203
	gat Asp 400									1251
	gtc Val									1299
	atg Met									1347
	tta Leu									1395
~ ~	aac Asn				_			 _		 1443
	aca Thr 480									1491
	tac Tyr									1539

aac gat ggg tot gtc ata tagatoggot gcgtktgcg Asn Asp Gly Ser Val Ile 1576

<210> 18

<211> 516

<212> PRT

<213> Zea mays

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile 1 5 10 15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro 50 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro 165 170 175

Pro Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln 210 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val 225 230 235 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr

245 250 255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn 260 265 270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala 275 280 285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys 290 295 300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp 305 310 315 320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln 325 330 335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser 340 345 350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp 355 360 365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro 370 375 380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp 385 390 395

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val 405 410 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met 420 425 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu 435 440 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn 450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr 485 490 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp 500 505

Gly Ser Val Ile 515

<210> 19

<211> 1576

<212> DNA

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<213> Zea mays
<220>
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<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable
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<222> (267)
\langle 223 \rangle k = g or t; amino acid 86 = Ala.
<221> variation
<222> (1008)
<223> y = c or t.
<220>
<221> variation
<222> (1209)
<223> y = c \text{ or t.}
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<221> variation
<222> (1368)
\langle 223 \rangle r = a or g; amino acid \langle 453 \rangle = Pro.
<221> variation
<222> (1371)
<223> h = a or c or t/u.
<220>
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<222> (1578)
<223> k = g or t.
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cag ata aga tot tgt gag ggt gat ggg att gac agg ttg gaa aaa tta
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                                                                      195
qqt qqt aqa gtt gct gca act aca caa tgt att ctt acc tca gat gct
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
             50
                                   55
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
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65 70 75

gct	gat	gca	aac	cgt	gta	tct	gck	atc	att	ttg	ggc	gga	ggc	act	gga	291
Ala	Asp 80	Ala	Asn	Arg	Val	Ser 85	Ala	Ile	Ile	Leu	Gly 90	Gly	Gly	Thr	Gly	
	~	ctc Leu			_		_		~	-	-		-	_		339
		gga Gly														387
		ggt Gly														435
_		aac Asn 145	_				_				_					483
		gat Asp														531
		gct Ala														579
		gta Val		-	_											627
_		ttg Leu	_		-											675
		aaa Lys 225														723
		gat Asp														771
		gga Gly														819
		tct Ser														867
gat	gca	cag	aaa	tat	сса	tac	ctt	gca	tca	atg	ggc	att	tat	gtc	ttc	915

Asp	Ala	Gln	Lys 290	Tyr	Pro	Tyr	Leu	Ala 295	Ser	Met	Gly	Ile	Tyr 300	Val	Phe	
_			_	ctt Leu		-			_							963
				tct Ser												1011
				att Ile												1059
				gat Asp 355												1107
	_			gat Asp												1155
				caa Gln												1203
				tta Leu												1251
				cgt Arg												1299
atg	atg	gga	gcg	gac	atc	tat	gaa	act	gaa	gaa	gaa	gct	tca	aag	cta	1347
Met	Met	Gly	Ala	Asp 435	Ile	Tyr	Glu	Thr	Glu 440	Glu	Glu	Ala	Ser	Lys 445	Leu	
				aag Lys												1395
				att Ile												1443
				aag Lys												1491
				tct Ser												1539
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Asn Asp Gly Ser Val Ile 515

<210> 20

<211> 516

<212> PRT

<213> Zea mays

<400> 20

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Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
50 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu 130 135 140

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro 165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln 210 215 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val 225 230 235 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr

255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn

245

260 265 270

250

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala 275 280 285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys 290 295 300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp 305 310 315

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln 325 330 335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser 340 345 350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp 355 360 365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro 370 375 380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser His 385 390 395 400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val 405 410 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met 420 425 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu  $435 \hspace{1.5cm} 440 \hspace{1.5cm} 445$ 

Ala Gly Lys Val Pro Ile Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn 450 450 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr 485 490 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp 500 505 510

Gly Ser Val Ile 515

<210> 21

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<212> DNA

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<213> Zea mays
<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
     heat stable
<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.
<221> variation
<222> (321)
<223> n = a or g or c or t/u, unknown, or other.
<220>
<221> variation
<222> (1008)
<223> y = c or t.
<220>
<221> variation
<222> (1368)
\langle 223 \rangle r = a or g; amino acid 453 = Pro.
<220>
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<222> (1578)
<223> k = g or t.
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                             5
                                                10
cag ata aga tot tgt gag ggt gat ggg att gac agg ttg gaa aaa tta
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15
                      20
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt
                                                                    147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                 35
                                                           45
ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct
                                                                    195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
             50
                                  55
                                                       60
tgt cet gaa act ett eat tet eaa aca eag tee tet agg aaa aat tat
                                                                    243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
                              70
                                                   75
get gat gea aac egt gta tet gek ate att ttg gge gga gge aet gga
                                                                    291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
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80		85	90		
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	a tgt tac agg y Cys Tyr Arg 115	_	-		
	t ata aat aag y Ile Asn Lys 130				
_	c cgc cat att n Arg His Ile 5	_	Tyr Leu Glu		
	t gga tct gta p Gly Ser Val				
	t gga tgg ttc a Gly Trp Phe 180				
	a ctc gag gat l Leu Glu Asp 195	_		_	
~	g agt ggc gat u Ser Gly Asp 210	-			
	a cat gtc gag s His Val Glu 5		Asp Ile Thr	_	_
	t gag agc cga o Glu Ser Arg	_			_
	a cgt gta ctt y Arg Val Leu 260		-		_
_	t atg aga gtt r Met Arg Val 275		5 5	_	_
	g aaa tat cca n Lys Tyr Pro 290				
	t gca ctt tta o Ala Leu Leu 5	-	Lys Ser Lys		

			gga Gly											1011
			tgc Cys											1059
			ttt Phe											1107
	-		tac Tyr 370	_										1155
			acg Thr											1203
			tgc Cys											1251
			tca Ser											1299
			gcg Ala											1347
_		_	ggg Gly 450	_	-		_							1395
			atc Ile											1443
			agt Ser											1491
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			tct Ser			taga	atcg	get g	gcgtl	ktgc	g			1576

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<212> PRT

<213> Zea mays

<400> 22

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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro 50 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
85 90 95

Leu Phe Pro Leu Thr Ser Thr Thr Ala Thr Pro Ala Val Pro Val Gly
100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro 165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln 210 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val 225 230 235 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr 245 250 255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn 260 265 270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala 275 280 285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys 295 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp 310 315 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln 325 330 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser 345 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro 375 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp 390 395 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val 410 405 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met 425 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn 455 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 470 475 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp 505 Gly Ser Val Ile 515

<210> 23

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<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunken-2 gene revertant form, modified to be heat stable

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<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.
<220>
<221> variation
<222> (1008)
<223> y = c or t.
<220>
<221> variation
<222> (1368)
\langle 223 \rangle r = a or g; amino acid 453 = Pro.
<220>
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<222> (1389)
<223> h = a or c or t/u.
<220>
<221> variation
<222> (1578)
<223> k = g \text{ or t.}
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caq ata aga tot tgt gag ggt gat ggg att gac agg ttg gaa aaa tta
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15
                                           25
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt
                                                                    147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct
                                                                    195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
                                  55
                                                                    243
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
qct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga
                                                                    291
Ala Asp Ala Asn Arq Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
tet eaq ete ttt eet etq aca age aca aga get acg eet get gta eet
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
                                         105
                                                              110
 95
                     100
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
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115 120 125

		115				120			125	
	 	aat Asn	_							435
		cat His								483
		tct Ser								531
		tgg Trp								579
		gag Glu 195								627
_	_	 ggc Gly		_						675
		gtc Val								723
		agc Ser								771
		 gta Val								819
		aga Arg 275								867
		tat Tyr								915
		ctt Leu								963
		 tct Ser					-			1011
		att Ile								1059

aaa t Lys S				_			_	_			-	_			-	1107
ttt g Phe A																1155
ttg c Leu E		-	_		_	_	_	_	_				-			1203
tca g Ser A																1251
gga g Gly V 415	_	-														1299
atg a Met M																1347
ctg t Leu I		_		_	_		_							_		1395
agg a Arg A																1443
atc a Ile 1																1491
tac t Tyr 1 495										_			-			1539
aac g Asn A						taga	ateg	get (	gegtl	ktgc	3					1576
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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile

<400> 24

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Arg	Val 50	Ala	Ala	Thr	Thr	Gln 55	Cys	Ile	Leu	Thr	Ser 60	Asp	Ala	Cys	Pro
Glu 65	Thr	Leu	His	Ser	Gln 70	Thr	Gln	Ser	Ser	Arg 75	Lys	Asn	Tyr	Ala	Asp 80
Ala	Asn	Arg	Val	Ser 85	Ala	Ile	Ile	Leu	Gly 90	Gly	Gly	Thr	Gly	Ser 95	Gln
Leu	Phe	Pro	Leu 100	Thr	Ser	Thr	Arg	Ala 105	Thr	Pro	Ala	Val	Pro 110	Val	Gly
Gly	Cys	Tyr 115	Arg	Leu	Ile	Asp	Ile 120	Pro	Met	Ser	Asn	Cys 125	Phe	Asn	Ser
Gly	Ile 130	Asn	Lys	Ile	Phe	Val 135	Met	Ser	Gln	Phe	Asn 140	Ser	Thr	Ser	Leu
Asn 145	Arg	His	Ile	His	Arg 150	Thr	Tyr	Leu	Glu	Gly 155	Gly	Ile	Asn	Phe	Ala 160
Asp	Gly	Ser	Val	Gln 165	Val	Leu	Ala	Ala	Thr 170	Gln	Met	Pro	Glu	Glu 175	Pro
Ala	Gly	Trp	Phe 180	Gln	Gly	Thr	Ala	Asp 185	Ser	Ile	Arg	Lys	Phe 190	Ile	Trp
Val	Leu	Glu 195	Asp	Tyr	Tyr	Ser	His 200	Lys	Ser	Ile	Asp	Asn 205	Ile	Val	Ile
Leu	Ser 210	Gly	Asp	Gln	Leu	Tyr 215	Arg	Met	Asn	Tyr	Met 220	Glu	Leu	Val	Gln
Lys 225	His	Val	Glu	Asp	Asp 230	Ala	Asp	Ile	Thr	Ile 235	Ser	Cys	Ala	Pro	Val 240
Asp	Glu	Ser	Arg	Ala 245	Ser	Lys	Asn	Gly	Leu 250	Val	Lys	Ile	Asp	His 255	Thr
Gly	Arg	Val	Leu 260	Gln	Phe	Phe	Glu	Lys 265	Pro	Lys	Gly	Ala	Asp 270	Leu	Asn
Ser	Met	Arg 275	Val	Glu	Thr	Asn	Phe 280	Leu	Ser	Tyr	Ala	Ile 285	Asp	Asp	Ala
Gln	Lys 290	Tyr	Pro	Tyr	Leu	Ala 295	Ser	Met	Gly	Ile	Tyr 300	Val	Phe	Lys	Lys
Asp 305	Ala	Leu	Leu	Asp	Leu 310	Leu	Lys	Ser	Lys	Tyr 315	Thr	Gln	Leu	His	Asp 320
Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arq	Ala	Val	Leu	Asp	Tyr	Ser	Val	Gln

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caq ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt
                                                                   147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct
                                                                   195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat
                                                                   243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
get gat gea aac egt gta tet gek ate att ttg gge gga gge aet gga
                                                                   291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
tet eag etc ttt eet etg aca age aca aga get acg eet get gta eet
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Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc
                                                                   387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
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Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
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                                135
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Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
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cat act gga cgt His Thr Gly Arg 255	_				819
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cat gac ttt gga His Asp Phe Gly 320					1011
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Leu	Phe	Pro	Leu 100	Thr	Ser	Thr	Arg	Ala 105	Thr	Pro	Ala	Val	Pro 110	Val	Gly
Gly	Cys	Tyr 115	Arg	Leu	Ile	Asp	Ile 120	Pro	Met	Ser	Asn	Cys 125	Phe	Asn	Ser
Gly	Ile 130	Asn	Lys	Ile	Phe	Val 135	Met	Ser	Gln	Phe	Asn 140	Ser	Thr	Ser	Leu
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Asp	Gly	Ser	Val	Gln 165	Val	Leu	Ala	Ala	Thr 170	Gln	Met	Pro	Glu	Glu 175	Pro
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Val	Leu	Glu 195	Asp	Tyr	Tyr	Ser	His 200	Lys	Ser	Ile	Asp	Asn 205	Ile	Val	Ile
Leu	Ser 210	Gly	Asp	Gln	Leu	Tyr 215	Pro	Met	Asn	Tyr	Met 220	Glu	Leu	Val	Gln
Lys 225	His	Val	Glu	Asp	Asp 230	Ala	Asp	Ile	Thr	Ile 235	Ser	Cys	Ala	Pro	Val 240
Asp	Glu	Ser	Arg	Ala 245	Ser	Lys	Asn	Gly	Leu 250	Val	Lys	Ile	Asp	His 255	Thr
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                                     410
Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
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Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
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Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
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Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
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Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt
                                                                    147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
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                                                                    195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat
                                                                    243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga
                                                                    291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
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                         85
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gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc
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Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
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Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
                                 135
tog oft aac ogo cat att cat ogt aca tac oft gaa ggo ggg atc aac
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Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
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		_			ttc Phe 180	_										579
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gat Asp aag Lys cat His gtg Val 335 aaa	Asn gca Ala aaa Lys gac Asp 320 cag Gln tca	cag Gln gat Asp 305 ttt Phe gca Ala	aaa Lys 290 gca Ala gga Gly tgc Cys	275 tat Tyr ctt Leu tct Ser att Ile	cca Pro tta Leu gaa Glu ttt	tac Tyr gac Asp atc Ile 325 acg Thr	ctt Leu ctt Leu 310 ctc Leu ggc Gly	Asn gca Ala 295 ctc Leu cca Pro tat Tyr	Phe 280 tca Ser aag Lys aga Arg tgg Trp	Leu atg Met tca ser gct Ala gag Glu 345 act	ggc Gly aaa Lys gta Val 330 gat Asp	att Ile tat Tyr 315 cta Leu gtt Val	tat Tyr 300 act Thr gat Asp	gtc Val caa Gln cay His aca Thr	ttc Phe tta Leu agt Ser atc Ile 350	963

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			gtc Val 420									1299
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			gtc Val									1395
			gac Asp									1443
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Val	Leu	Glu 195	Asp	Tyr	Tyr	Ser	His 200	Lys	Ser	Ile	Asp	Asn 205	Ile	Val	Ile
Leu	Ser 210	Gly	Asp	Gln	Leu	Tyr 215	Arg	Met	Asn	Tyr	Met 220	Glu	Leu	Val	Gln
Lys 225	His	Val	Glu	Asp	Asp 230	Ala	Asp	Ile	Thr	Ile 235	Ser	Cys	Ala	Pro	Val 240
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Ser	Met	Arg 275	Val	Glu	Thr	Asn	Phe 280	Leu	Ser	Tyr	Ala	Ile 285	Asp	Asp	Ala
Gln	Lys 290	Tyr	Pro	Tyr	Leu	Ala 295	Ser	Met	Gly	Ile	Tyr 300	Val	Phe	Lys	Lys
Asp 305	Ala	Leu	Leu	Asp	Leu 310	Leu	Lys	Ser	Lys	Tyr 315	Thr	Gln	Leu	His	Asp 320
Phe	Gly	Ser	Glu	Ile 325	Leu	Pro	Arg	Ala	Val 330	Leu	Asp	His	Ser	Val 335	Gln
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Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
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Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct
                                                                    195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
             50
                                  55
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                                                                    243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
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                              70
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                          85
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Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
95
                    100
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gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc
                                                                    387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
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                115
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act
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Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
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-		_	_		gat Asp											675
					gag Glu											723
	-			_	cga Arg	_							-		-	771
					ctt Leu 260											819
_			_	_	gtt Val	~ ~				_	_		_		-	867
_		_			cca Pro					_				_		915
					tta Leu											963
					aar Lys						-		-	_	_	1011
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Ala	Asn	Arg	Val	Ser 85	Ala	Ile	Ile	Leu	Gly 90	Gly	Gly	Thr	Gly	Ser 95	Gln
Leu	Phe	Pro	Leu 100	Thr	Ser	Thr	Arg	Ala 105	Thr	Pro	Ala	Val	Pro 110	Val	Gly
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Asn 145	Arg	His	Ile	His	Arg 150	Thr	Tyr	Leu	Glu	Gly 155	Gly	Ile	Asn	Phe	Ala 160
Asp	Gly	Ser	Val	Gln 165	Val	Leu	Ala	Ala	Thr 170	Gln	Met	Pro	Glu	Glu 175	Pro
Ala	Gly	Trp	Phe 180	Gln	Gly	Thr	Ala	Asp 185	Ser	Ile	Arg	Lys	Phe 190	Ile	Trp
Val	Leu	Glu 195	Asp	Tyr	Tyr	Ser	His 200	Lys	Ser	Ile	Asp	Asn 205	Ile	Val	Ile
Leu	Ser 210	Gly	Asp	Gln	Leu	Tyr 215	Arg	Met	Asn	Tyr	Met 220	Glu	Leu	Val	Gln
Lys 225	His	Val	Glu	Asp	Asp 230	Ala	Asp	Ile	Thr	Ile 235	Ser	Cys	Ala	Pro	Val 240
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Gln	Lys 290	Tyr	Pro	Tyr	Leu	Ala 295	Ser	Met	Gly	Ile	Tyr 300	Val	Phe	Lys	Lys
Asp 305	Ala	Leu	Leu	Asp	Leu 310	Leu	Lys	Ser	Lys	Tyr 315	Thr	Gln	Leu	His	Asp 320
Phe	Gly	Ser	Lys	Ile 325	Leu	Pro	Arg	Ala	Val 330	Leu	Asp	His	Ser	Val 335	Gln
Ala	Cys	Ile	Phe 340	Thr	Gly	Tyr	Trp	Glu 345	Asp	Val	Gly	Thr	Ile 350	Lys	Ser
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Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
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ctg Leu																1395
agg Arg																1443
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				ctt Leu							387
				ata Ile							435
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		 	_	cag Gln 165							531
				cag Gln							579
				tat Tyr							627
				cag Gln							675
				gac Asp							723
				gct Ala 245							771

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						tac Tyr								915
						gac Asp								963
						atc Ile 325								1011
						acg Thr								1059
						aac Asn								1107
	_			_		aaa Lys				_		-	-	1155
						gac Asp								1203
						aga Arg 405								1251
						agc Ser								1299
						tat Tyr								1347
						ccr Pro								1395
		_			_	atg Met	***			-				1443

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tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539

Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile 500 505 510

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Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
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Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu 130 140

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Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro 165 170 175

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Asp Glu Ser Arg	Ala Ser Lys 245	Asn Gly Leu 250	Val Lys Ile	Asp His Thr 255
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Ser Met Arg Val 275	Glu Thr Asn	Phe Leu Ser 280	Tyr Ala Ile 285	Asp Asp Ala
Gln Lys Tyr Pro 290	Tyr Leu Ala 295	Ser Met Gly	Ile Tyr Val 300	Phe Lys Lys
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Phe Gly Ser Glu	Ile Leu Pro 325	Arg Ala Val 330	Leu Asp Met	Ser Val Gln 335
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Phe Tyr Asp Pro	Lys Thr Pro 375	Phe Phe Thr	Ala Pro Arg 380	Cys Leu Pro
Pro Thr Gln Leu 385	Asp Lys Cys 390	Lys Met Lys	Tyr Ala Phe 395	Ile Ser Asp 400
Gly Cys Leu Leu		Asn Ile Glu 410		Ile Gly Val 415
Cys Ser Arg Val 420	Ser Ser Gly	Cys Glu Leu 425	Lys Asp Ser	Val Met Met 430
Gly Ala Asp Ile 435	Tyr Glu Thr	Glu Glu Glu 440	Ala Ser Lys 445	Leu Leu Leu
Ala Gly Lys Val 450	Pro Val Gly 455	Ile Gly Arg	Asn Thr Lys 460	Ile Arg Asn
Cys Ile Ile Asp 465	Met Asn Ala 470	Arg Ile Gly	Lys Asn Val 475	Val Ile Thr 480
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			tct Ser 85					291
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			ctt Leu					387
			ata Ile					435
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			cag Gln 165					531
			cag Gln					579
			tat Tyr					627
_			cag Gln				_	675
			gac Asp					723
			gct Ala 245					771
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		c tat tgg gag gat y Tyr Trp Glu Asp 345	
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	_	a act gaa gaa gaa u Thr Glu Glu Glu 440	
		t gga ata gga agg 1 Gly Ile Gly Arg 455	
		t gct agg att ggg n Ala Arg Ile Gly 0	
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Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
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Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser 115 120 125

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Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
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Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile 195 200 205

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Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val 225 230 235 240

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Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
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Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
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						tat Tyr										627
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						gac Asp										723
	_	_		_	_	gct Ala 245							_		-	771
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						gag Glu										867
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Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp 65 70 75 80

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Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro 165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln 210 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val 225 230 235 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr 245 250 255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn 260 265 270

510

Ser Met Arq Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys 295 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp 310 315 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln 330 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp 360 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro 375 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp 390 395 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val 410 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu 440 445 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 470 475 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr 490

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<222> (540)
<223> n = a or g or c or t/u, unknown, or other.
<221> variation
<222> (1008)
<223> y = c or t.
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Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt
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Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
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                                                                   195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat
                                                                   243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
get gat gea aac egt gta tet gek ate att tig gge gga gge aet gga
                                                                   291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
                         85
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	cag Gln				-								339
_	gga Gly						-			_	_	_	387
	agt Ser												435
	ctt Leu												483
	gct Ala 160												531
	cca Pro	_				_		-	-				579
	tgg Trp												627
_	atc Ile	_	-	-	_	_							675
-	cag Gln												723
	gtt Val 240												771
	act Thr												819
	aat Asn												867
_	gca Ala	_					-						915
	aaa Lys	_	_			-		_					963

cat g His A 3	•				-									1011
gtg c Val G 335	_	-	_								-	-		1059
aaa t Lys S				_	-									1107
ttt g Phe A	,											-	_	 1155
ttg c Leu P														1203
tca g Ser A														1251
gga g Gly V 415														1299
atg a Met M														1347
ctg t Leu I														1395
agg a Arg A														1443
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- Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly 40 45
- Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro 50 60
- Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp 65 70 75 80
- Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
  85 90 95
- Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
- Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser 115 120 125
- Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu 130 135 140
- Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala 145 150 155 160
- Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro 165 170 175
- Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp 180 185 190
- Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile 195 200 205
- Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln 210 215 220
- Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val 225 230 235 240
- Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr 245 250 255
- Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn 260 265 270
- Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala 275 280 285
- Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys

290 295 300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp 305 310 315 320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln 325 330 335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser 340 345 350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp 355 360 365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro 370 380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp 385 390 395 400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val 405 410 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met 420 425 430

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Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn 450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 465 470 475 480

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<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunken-2 gene revertant form, modified to be heat stable

<220>

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<221> variation
<222> (267)
\langle 223 \rangle k = g or t; amino acid 86 = Ala.
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Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
15
                     20
                                          25
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                 35
qqt qqt aqa qtt qct qca act aca caa tqt att ctt acc tca qat qct
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
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tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
         65
get gat gea aac egt gta tet gek ate att ttg gge gga gge aet gga
                                                                    291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
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tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
95
                    100
                                         105
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aac agt Asn Sei	Gly I											435
tcg ctt Ser Lei												483
ttt gct Phe Ala 160	Asp G											531
gag cca Glu Pro 175												579
atc tgg Ile Trp			u Asp									627
gta ato Val Ile	Leu S		-	-								675
gtg cag Val Glr												723
cct gtt Pro Val 240	. Asp G											771
cat act His The 255	Gly A	Arg Va		Gln	Phe	Phe	Glu	Lys	Pro			819
ttg aat Leu Asr			g Val									867
gat gca Asp Ala	Gln I											915
aag aaa Lys Lys		_		-								963
cat gad His Asp 320	Phe G											1011

gtg cag g Val Gln A 335											1059
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ttt gat t Phe Asp P	-	•							_	_	1155
ttg cct c Leu Pro P 3			Asp Ly								1203
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gga gtc t Gly Val C 415											1299
atg atg g Met Met G	Sly Ala A										1347
ctg tta g Leu Leu A											1395
agg aac t Arg Asn C 4	_	-	Met A								1443
atc aca a Ile Thr A 480											1491
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Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala 275 280 285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys

300

295

290

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp 310 315 305 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln 330 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser 345 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp 355 360 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro 375 380 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp 385 390 395 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu 435 440 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn 455 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 465 470 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr 490 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp 505 510 Gly Ser Val Ile 515